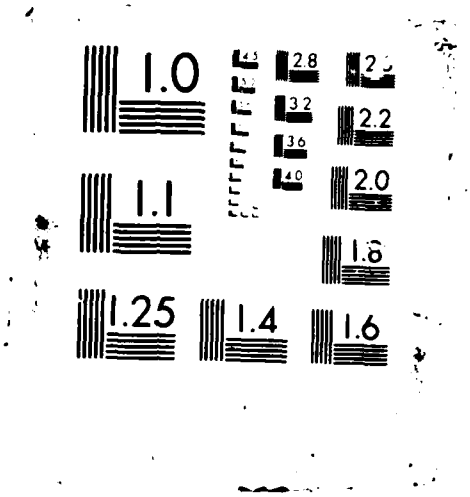
AD-A176 359 COMPUTATIONAL APPROACHES TO PROTEIN STRUCTURE DESIGN: 1/1
BETA-BELLIN(U) MASSACHUSETTS GENERAL HOSPITAL BOSTON
J NOVOTNY 26 JAN 87 N00014-86-K-0116

UNCLASSIFIED F/G 6/1 NL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REPORT DOCUMENTATION PAGE

1a REPORT SECURITY CLASSIFICATION: (U)	1b RESTRICTIVE MARKINGS: NA
2a SECURITY CLASSIFICATION AUTHORITY: NA	3 DISTRIBUTION / AVAILABILITY OF REPORT: Distribution unlimited
2b DECLASSIFICATION / DOWNGRADING SCHEDULE: NA	
4 PERFORMING ORGANIZATION REPORT NUMBER(S): Massachusetts General Hospital/Harvard Med.Sch	5 MONITORING ORGANIZATION REPORT NUMBER(S): NA
6a NAME OF PERFORMING ORGANIZATION: Massachusetts General Hospital; 6b OFFICE SYMBOL (If applicable): NA	7a NAME OF MONITORING ORGANIZATION: Office of Naval Research
6c ADDRESS (City, State, and ZIP Code): MAssachusetts General Hospital Jackson 13, Boston MA 02114	7b ADDRESS (City, State, and ZIP Code): 800 N. Quincy Street Arlington VA 22217-5000
8a NAME OF FUNDING / SPONSORING ORGANIZATION: Office of Naval Research; 8b OFFICE SYMBOL (If applicable): ONR	9 PROCUREMENT INSTRUMENT IDENTIFICATION NUMBER: N00014-86-K-0116
8c ADDRESS (City, State, and ZIP Code): 800 N. Quincy Street Arlington VA 22217-5000	10 SOURCE OF FUNDING NUMBERS: PROGRAM ELEMENT NO 61153N; PROJECT NO RR04106; TASK NO; WORK UNIT ACCESSION NO

11 TITLE (Include Security Classification)

(U) Computational Approaches to Protein Structure Design: beta-Bellin

12 PERSONAL AUTHOR(S)

Novotny, Jiri

13a TYPE OF REPORT	13b TIME COVERED	14 DATE OF REPORT (Year, Month, Day)	15 PAGE COUNT
Annual	FROM 2/1/86 TO 1/30/87	1/26/1987	6

16 SUPPLEMENTARY NOTATION

17 COSATI CODES			18 SUBJECT TERMS (Continue on reverse if necessary and identify by block number)
FIELD	GROUP	SUB-GROUP	
08			Protein engineering, 3D structure. Molecular dynamics

19 ABSTRACT (Continue on reverse if necessary and identify by block number)

Computer analysis of protein models is used to aid design of new protein structures. Using atomic coordinates of beta-bellin, an antiparallel beta-sheeted protein model designed by Jane & David Richardson, charactersitcs such as solvent-accessible surface, polypeptide backbone twist, beta-barrel geometry, empirical potential energy etc. were computed and compared with values obtained from atomic coordinates of native proteins. This approach involves computer analysis of native proteins as well. In addition to static molecular properties, dynamical behavior of native proteins and protein models is compared using molecular dynamics calculations.

20 DISTRIBUTION / AVAILABILITY OF ABSTRACT	21 ABSTRACT SECURITY CLASSIFICATION
☐ UNCLASSIFIED/UNLIMITED ☐ SAME AS RPT ☐ DTIC USERS	(U)
22a NAME OF RESPONSIBLE INDIVIDUAL: M. Marron	22b TELEPHONE (Include Area Code): 617-726-1858; 22c OFFICE SYMBOL: ONR

DD FORM 1473, 84 MAR — 83 APR edition may be used until exhausted. All other editions are obsolete. SECURITY CLASSIFICATION OF THIS PAGE

Annual report on "Computational Approaches to Protein Structure Design: β-Bellin.

The goals of this project are to aid design of new protein structures by computer analysis of protein models. Using atomic coordinates of β-bellin, an antiparallel β-sheeted protein model designed by Drs. Jane & David Richardson, characteristics such as solvent-accessible surface, polypeptide backbone twist, b-barrel geometry (semiaxes of hyperboloidal cross-sections), empirical potential energy etc. were computed and compared with values obtained from atomic coordinates of native proteins. This approach involves computer analysis of native proteins as well. In addition to static molecular properties, dynamical behavior of native proteins and protein models is compared using molecular dynamics calculations.

In the first year of the project, computer analysis of native proteins concentrated on backbone twist of β-sheets and solvent- or large probe-accessible surfaces of selected proteins. Analysis of backbone twists showed large deviations from the average β-strand twist value of +20°. The deviations correlate with anisotropy of non-covalent atomic force distribution throughout the structure. Large probe-accessible surfaces of enzymes were shown to coincide with sites of limited autolysis/proteolysis.

Backbone twist and solvent accesible surface of the β-bellin model were computed and compared to those of native proteins of similar molecular weight and architecture. Quenched molecular dynamics (i.e., a molecular dynamics simulation at 800°K followed by a gradual cooling of the structure) over 10 ps resulted in partial unfolding of the model. More detailed dynamical investigation, at various temperatures (including 300°K) and on improved models, is currently under way.

One paper has been published as a result of this work. Reprints will be sent under separate cover.

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